

Amendments to the Claims

Please amend the claims as follows:

1. (currently amended) A method of identifying a relationship between one or more candidate biomolecules and multiple reference biomolecules, the method comprising:

(a) inputting to a computer a query set describing the one or more candidate biomolecules;

(b) comparing the query set with a target database describing the multiple reference biomolecules, wherein the multiple reference biomolecules are grouped into one or more buckets, and wherein the reference biomolecules of each bucket share a common property;

(c) counting a number of matches between each query set and each bucket of the target database; ~~and~~

(d) statistically analyzing each match to identify, ~~wherein the presence of a statistically significant matches;~~

(e) sorting the results of step (d) by increasing or decreasing significance; and

(f) displaying the results to a user, where said statistically significant matches identify ~~identifies~~ a relationship between the query set and a bucket of the target database.

2. (currently amended) The method of claim 1, wherein the query set comprises one or more sequences selected from the group consisting of DNA sequences, RNA sequences, and protein sequences.

3. (cancel)

4. (original) The method of claim 2, wherein the one or more sequences are extracted from one genetic region.

5. (previously presented) The method of claim 1, wherein the one or more candidate biomolecules and the multiple reference biomolecules are all selected from the group consisting of proteins, nucleic acids, and small molecules.

6. (original) The method of claim 1, wherein the comparing comprises employing an equivalence algorithm based on identity of name, accession, or other identifier associated with biomolecule.

7. (currently amended) The method of claim 2 ~~claim 1~~, wherein the comparing comprises employing a BLAST-based algorithm to identify similarities or identities in two or more sequences.

8. (currently amended) The method of claim 2 ~~claim 1~~, wherein the counting comprises applying one or more principles chosen from the group consisting of: (a) each query set candidate sequence can match at most one reference sequence in any given bucket; (b) each query set candidate sequence can possess a match in one or more different buckets; and (c) once a candidate sequence in the query set matches a specific bucket reference sequence in the target database, any subsequent matches of that same candidate sequence to other reference sequences in that bucket do not increase the match count for the bucket.

9. (original) The method of claim 1, wherein the statistically analyzing comprises computing one or more statistics for each bucket.

10. (currently amended) The method of claim 9 ~~claim 8~~, further comprising sorting the one or more statistics by increasing or decreasing significance.

11. (original) The method of claim 1, further comprising outputting a webpage with results of the statistical analysis, the webpage comprising one or more hyperlinks.

12. -66 cancel.